Spatial Capture-Recapture Workshop

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Workshop logistics

- Each morning: Coffee and food
- Coffee breaks: mid-morning, mid-afternoon. Come and go as you wish.
- Lunch: 12:30ish
- We'll work until 5:00 or so.
- Wireless internet:
 - RedRover

The book

Spatial Capture-Recapture

J. Andrew Royle • Richard B. Chandler • Rahel Sollmann • Beth Gardner

Spatial Capture-Recapture provides a revolutionary extension of traditional capture-recapture methods for studying animal populations using data from live trapping, camera trapping, DNA sampling, acoustic sampling, and related field methods. This book is a conceptual and methodological synthesis of spatial capture-recapture modeling. As a comprehensive how-to manual, this reference contains detailed examples of a wide range of relevant spatial capture-recapture models for inference about population size and spatial and temporal variation in demographic parameters. Practicing field biologists studying animal populations will find this book to be a useful resource, as will graduate students and professionals in ecology, conservation biology, and fisheries and wildlife management.

Key features:

- · Offers comprehensive coverage of revolutionary new methods in ecology
- Includes detailed worked examples with R and BUGS code for each methodological element along with software instructions and a companion R package so you can implement analyses and learn by doing
- · Presents a practical approach, embracing Bayesian and classical inference strategies in order to provide a variety of options to best get the job done



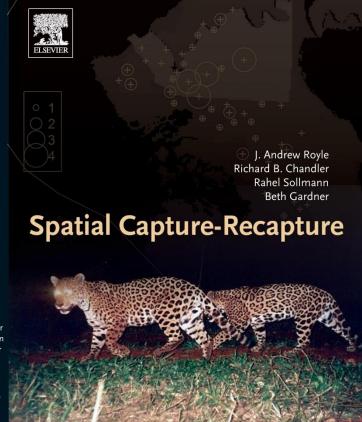














The website and email list

SCR website:

https://sites.google.com/site/spatialcapturerecapture/

- R package scrbook
- R package SCRbayes

SCR email list:

https://groups.google.com/forum/#!forum/spatialcapturerecapture

Sign up!

SEND FEEDBACK AND SUGGESTIONS

Email: hmecology@gmail.com or directly to aroyle@usgs.gov or jaroyle@gmail.com (profane comments here)

This is an intermediate-level workshop with topical lectures followed by work sessions involving data analysis. Course requirements:

- Good working knowledge of modern regression methods (regression, ANOVA, generalised linear models, random effects).
- Experience with the R programming language at a level **higher** than "beginner". You should be a regular R user. Manipulating data in R should be routine for you.
- Knowledge of basic capture-recapture concepts and methods. E.g., the Otis et al. monograph, distance sampling, program MARK, etc.
- You should have heard of WinBUGS or JAGS. We will spend most of the first day learning how to fit basic regression, GLM and ordinary closed population models in WinBUGS.

OUTLINE OF THE WORKSHOP

Day 1:

- Attempt to motivate need and interest in SCR models
- BUGS/JAGS introduction
- Closed population models, and especially Bayesian analysis of them in BUGS/JAGS using "data augmentation"

Day 2:

- CR models with individual covariates: model Mx
- SCR models in BUGS/JAGS

Day 3:

- Likelihood analysis ideas
- Non-Euclidean distance models (connectivity)
- Open populations

Questions?

Introductions

Who are you? Where are you from? What do you do for a living?

Why do you care about SCR models?

INTRODUCTION: Why SCR?



Why SCR?

1. We care about N (or density, D)

AND ordinary CR models suffer a number of technical limitations

2. We care about spatial processes in ecology

movement space usage/resource selection connectivity spatial patterns in density

SCR unifies these two themes.

3. Efficient use of spatial data! New technologies allow study of species by CR that simply could not have been studied a few years ago. Rare species produce sparse data and we need to use all the data we have!

SCR enables us to study problems in spatial ecology with cheap encounter history data.

N

- At a fundamental level ecology is about understanding variability in N (spatial, temporal)
- Conservation and management: decisions depend on population size! (how many ducks/pumas/grizzlies are there?)
- Therefore: Estimating population size, N, is problem #1 in applied ecology

CAPTURE-RECAPTURE METHODS

CR models: estimating N and other population parameters (survival, recruitment, movement) from individual-level encounter history data == record of when individuals are captured == a sequence of 1's and 0's:

e.g., (1, 0, 1, 1, 0, 0) or (A, 0, B, B, 0, 0) for "2 states" etc...

- Long history of use in ecological sciences (Lincoln-Peterson estimator, 1930s, work by Don Hayne et al. 1940s and 1950s, small mammal studies, band recovery models, multi-state models in North American waterfowl populations)
- Major extensions and syntheses in 1970s-1980s: Jolly-Seber models (1965), Arnason (1972, 1973) multi-state models, books and monographs: Otis et al. 1978; Brownie et al. 1978; Seber 1982; White et al. 1982; and many others.

CLOSED POPULATION MODELS

- The existing framework (M0, Mt, Mb, Mh) was developed and synthesized in the 1970s (Otis et al. 1978).
- Design: repeated sampling of a CLOSED population of size
 N, we can estimate N from a sample of n individuals
- Heuristic: Nhat = n/\bar{p}

where $\bar{p} = Pr(captured during K occasions)$

• Process: estimate \bar{p} from a bunch of models, pick the best model, plug in to Heuristic Estimator and get Nhat

PROBLEMS WITH CLOSED POPULATION MODELS

- 1. They don't produce direct estimates of density, just population size relevant to some unknown area
- 2. Heterogeneous encounter probability: Individuals in the population should have a different probability of encounter depending on the location of their home range relative to traps.
- 3. Trap arrays can't have "holes" can be impractical from a design standpoint.

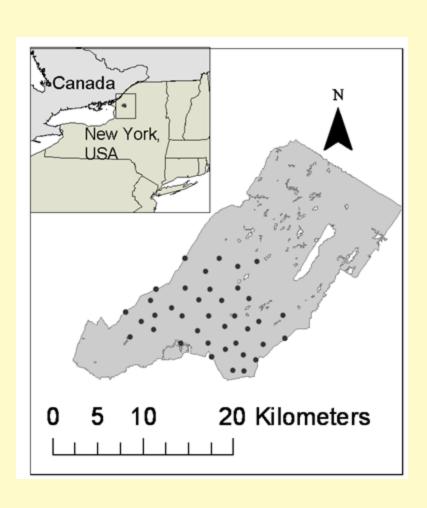
Problem 1: density and sample area

■ N is less ecologically relevant than is density (D), but they are related:

$$D = N/AREA$$

■ Cannot easily convert N to D in typical situations because the "area sampled" is not precisely defined.

Fort drum black bear data

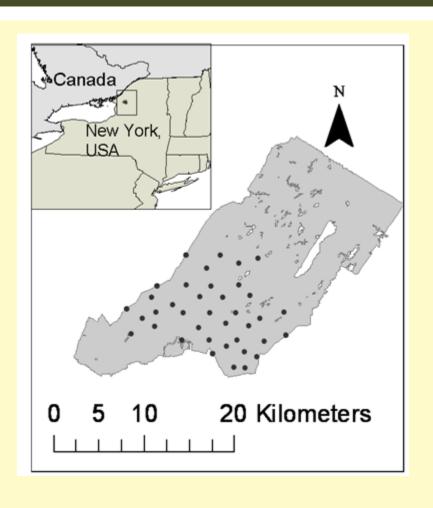


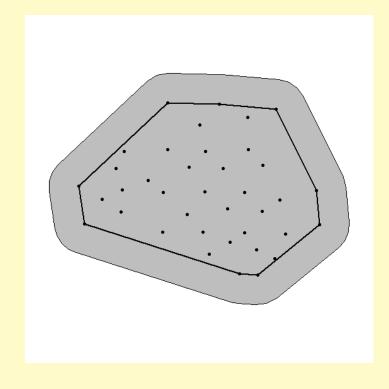
- I can get \widehat{N} from any closed population model.
- Does it apply to Fort Drum? Or a convex hull around the traps? Or where?
- The spatial context is important and CR models don't help us with that
- Fish bowl sampling

Problem 1: Sample area?

- Many methods for prescribing something akin to "effective sample area" have been proposed
- Put a buffer around the trap array.
 - But the trap array is a set of discrete points? Ok, so lets use a convex hull or similar to define the array, and then buffer the convex hull.
 - Buffer = how wide should the buffer be? Should be about .5 the typical home range size (Dice 1938). Or maybe 1x the home range size. Get an estimate of that from the literature. Or use the "mean maximum distance moved"(Wilson and Anderson 1985)

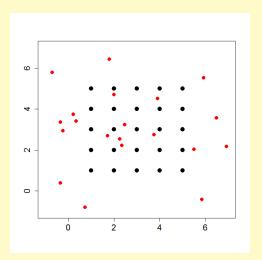
Fort drum study area, buffered

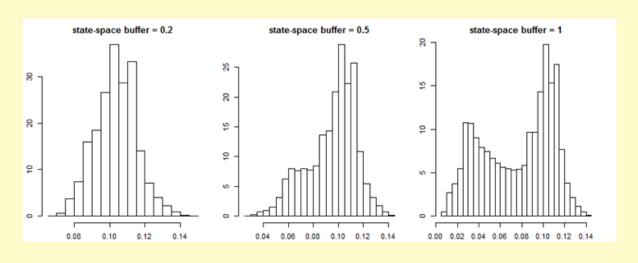




Problem 2: Heterogeneous detection

- Juxtaposition of individuals with traps induces a type of heterogeneity in encounter probability
- i.e., each individual has its own p. Individuals exposed to more traps have higher p, and vice versa.
- As individual home ranges move further from the trap array, p decreases toward 0





Problem 2: Heterogeneous detection

 Historically this has been accommodated by using "model Mh" (Karanth and Nichols papers)

What is Model Mh? h="heterogeneity" – each individual has it's own personal encounter probability

- Logit-normal: logit(p[i]) ~ Normal(mu, sigma^2)
- Finite mixture models (Norris and Pollock 1996; Pledger 2000)
- More recently: Individual covariate "distance to edge" (DTE) (Huggins 1991; Boulanger and McLellan 2001)
- Temporary emigration: adjust for heterogeneous detection using telemetry data

Problem 3: no holes in the array

Trapping arrays cannot have "holes":

- hole = space where animals aren't exposed to trapping
- Creates individuals with p = 0
- Estimated N does not apply to buffered area then
- Design: trap spacing should be about .5 home range radius

S.O.P. AS OF 2000-200X

- Karanth and Nichols papers....
 - Buffer by .5 MMDM to get "Area"
 - use N estimate from Model Mh (or Otis et al. 1978 suite of models)
 - D = Nhat/Area
- G. White (T Shenk and J. Ivan), Boulanger and McClellan (2001): Temporary emigration and individual covariate models (plus buffer)
- Boulanger and McClellan (2001) paper is a conceptual bridge between classical non-spatial CR and SCR models

Why all of this?

- Existing capture-recapture models apply to "fish-bowl" populations, that have no spatial dimension.
- All real studies generate spatial locations of capture. Since the dawn of time, this information has been discarded.
- Ordinary CR models don't use this data and so we have to conjure up methods of dealing with spatial explicitness using fish-bowl models
- We will see that SCR models resolve these technical limitations of fish-bowl models by extending ordinary CR models



2. WE CARE ABOUT SPATIAL PROCESSES IN ECOLOGY

- Distribution and abundance
- Connectivity of the landscape (corridor and reserve design)
- Resource selection or space usage
- Movement models

INTEGRATING THEORY WITH CAPTURE-RECAPTURE

- Historically capture-recapture dealt with "sampling" or "observation" processes, never "ecological process"
- This is because the ecological processes are mostly spatial, and the spatial dimension of CR data was summarized out or discarded
- If we retain the encounter location information in the model then we can build explicit hypotheses about space usage into CR models.

3. EFFICIENT USE OF SPATIAL DATA

- Existing capture-recapture models apply to fish bowl populations that have no spatial dimension
- All real studies generate spatial locations of capture. Historically, this information has been discarded. Maybe it is useful for something?
- SCR models allow us to use this spatial information.
 - Trap effects (effort)
 - Trap x time effects (behavioral response)

3. EFFICIENT USE OF SPATIAL DATA

- Encounter histories are "space x time" not just when but also where individuals are captured.
- Recaptures can happen during the same sampling occasion.
 CR models discard these.
- SCR models are all about retaining the where information.
- Trap specific effects (effort, variable operation, behavioral response)
- Affords greater design flexibility, staggered sampling.

NEW TECHNOLOGY

- New methods for obtaining individual encounter history data:
 - Camera trapping
 - Genetic sampling (hair snares, or dogs picking up scat,)
 - Acoustic sampling
 - PIT tags









NEW TECHNOLOGY

- New technologies are having a profound impact on the conduct of capture-recapture studies
 - Can study species that were not practical to study by capturerecapture 20 years ago (too rare, impossible to catch, expensive to catch, dangerous to handle)
 - Can do it reasonably cheap (and getting cheaper)

SUMMARY: WHY SCR?

- Resolves technical problems: Heterogeneity, "sample area", "holes"
- Integrate ecological theory with encounter history data. Space usage, connectivity, movement.
- Make use of spatial information in the data to properly specify models for individual encounter history data. i.e., models that use all 3 dimensions [individual, TIME, SPACE]
- New technologies producing vast amounts of spatial data that we toss out in order to use fish bowl models.

WHERE DID SCR MODELS COME FROM?

Distance sampling

■ Efford, M. (2004). Density estimation in live-trapping studies. *Oikos*, 106(3), 598-610.

connection between DS and a latent variable "s" == individual home range centroid. "inverse prediction"

■ Borchers, D. L., & Efford, M. G. (2008). Spatially explicit maximum likelihood methods for capture–recapture studies. *Biometrics*, 64(2), 377-385.

formal likelihood analysis

■ Royle, J. A., & Young, K. V. (2008). A hierarchical model for spatial capture-recapture data. *Ecology*, 89(8), 2281-2289.

Bayesian analysis, "area search" models

■ Royle, J. A. (2009). Analysis of capture–recapture models with individual covariates using data augmentation. *Biometrics*, 65(1), 267-274.

HOW DO WE ANALYZE SCR MODELS?

- Likelihood methods (R package "SECR" and some custom R code)
- SECR
 - Helper functions to package all of your data up
 - Model fitting functions
 - Summary functions
- Some types of models aren't in SECR and so we use our own R code for that.
- Bayesian analysis using WinBUGS/JAGS and some custom R code.
- Why should we use one or the other? Flexibility. Efficiency.

WHAT'S NEXT?

- Short course using BUGS / JAGS
- Closed population capture-recapture models (in BUGS, using data augmentation)